et al. (1997) Cell 89:1133-44); the AT-HOOK family (Reeves and Nissen (1990) Journal of Biological Chemistry 265:8573-8582); the S1FA family (Zhou et al. (1995) Nucleic Acids Res. 23:1165-1169); the bZIPT2 family (Lu and Ferl (1995) Plant Physiol. 109:723); the YABBY family (Bowman et al. (1999) Development 126:2387-96); the PAZ family (Bohmert et al. (1998) EMBO J. 17:170-80); a family of miscellaneous (MISC) transcription factors including the DPBF family (Kim et al. (1997) Plant J. 11:1237-1251) and the SPF1 family (Ishiguro and Nakamura (1994) Mol. Gen. Genet. 244:563-571); the golden (GLD) family (Hall et al. (1998) Plant Cell 10:925-936).

In the Claims:

Please **cancel** claims 17-36 without prejudice, and

Please **insert** new claims 37-76, as follows:

--37. (New) A transgenic plant comprising a recombinant polynucleotide comprising a nucleotide sequence encoding a transcription factor comprising a conserved domain of a plant AP2 transcription factor, wherein said transcription factor has at least 42% sequence identity with the AP2 transcription factor of SEQ ID NO: 18, and wherein said transgenic plant has enhanced tolerance to plant disease due to changes in expression levels or activity of said transcription factor.

38. (New) The transgenic plant of claim 37, wherein said conserved domain comprises:

an amino acid sequence of residues 145-213 of SEQ ID NO: 18;

an amino acid sequence having at least 84% identity to residues 145-213 of SEQ ID NO: 18; or

an amino acid sequence of residues 145-213 of SEQ ID NO: 18 having one or more conservative substitutions, deletions, or insertions.

39. (New) The transgenic plant of claim 37, wherein the recombinant polynucleotide comprises SEQ ID NO: 17.

40. (New) The transgenic plant of claim 37, wherein the recombinant polynucleotide further comprises one or more regulatory sequences.

41. (New) The transgenic plant of claim 40, wherein said one or more regulatory sequences are selected from the group consisting of a promoter, a transcription initiation start site, an RNA processing signal, a transcription termination site, and a polyadenylation signal.

42. (New) The transgenic plant of claim 41, wherein the selected promoter is constitutive, inducible, or tissue-specific.

43. (New) The transgenic plant of claim 37, wherein the nucleotide sequence encodes a polypeptide of SEQ ID NO: 18, wherein expression of the recombinant polynucleotide enhances the plant's tolerance to fungal disease when compared with the same trait of another plant of the same species lacking the recombinant polynucleotide.

44. (New) The transgenic plant of claim 43, wherein said fungal disease is caused by *Fusarium*, *Erysiphe, Sclerotinia* or *Botrytis*.

45. (New) A method for enhancing the disease tolerance or resistance of a plant comprising transforming a plant with a recombinant polynucleotide comprising a nucleotide sequence encoding a transcription factor comprising a conserved domain of a plant AP2 transcription factor, wherein said transcription factor has at least 42% sequence identity with the AP2 transcription factor of SEQ ID NO: 18, and wherein said transgenic plant has enhanced tolerance to plant disease due to changes in expression levels or activity of said plant transcription factor.

46. (New) The method of claim 45, wherein said conserved domain comprises:

an amino acid sequence of residues 145-213 of SEQ ID NO: 18;

an amino acid sequence having at least 84% identity to residues 145-213 of SEQ ID NO: 18; or

an amino acid sequence of residues 145-213 of SEQ ID NO: 18, having one or more conservative substitutions, deletions, or insertions.

47. (New) The method of claim 45, wherein the recombinant polynucleotide comprises SEQ ID NO: 17.

48. (New) The method of claim 45, wherein the recombinant polynucleotide further comprises one or more regulatory sequences.

10 ~~49.~~ (New) The method of claim 9 ~~48~~, wherein said one or more regulatory sequences are selected from the group consisting of a promoter, a transcription initiation start site, an RNA processing signal, a transcription termination site, and a polyadenylation signal.

11 ~~50.~~ (New) The method of claim 10 ~~49~~, wherein the selected promoter is constitutive, inducible, or tissue-specific.

51 (New) The method of claim 45, wherein the nucleotide sequence encodes a polypeptide of SEQ ID NO: 18, wherein expression of the recombinant polynucleotide enhances the plant's tolerance to fungal disease when compared with the same trait of another plant of the same species lacking the recombinant polynucleotide.

52. (New) The transgenic plant of claim 51, wherein said fungal disease is caused by *Fusarium*, *Erysiphe, Sclerotinia* or *Botrytis*.

53. (New) A method for altering the expression levels of at least one gene in a plant comprising transforming the plant with a recombinant polynucleotide comprising a nucleotide sequence encoding a transcription factor comprising a conserved domain of a plant AP2 transcription factor, wherein said transcription factor has at least 42% sequence identity with the AP2 transcription factor of SEQ ID NO: 18, and wherein said transgenic plant has enhanced tolerance to plant disease due to changes in expression levels or activity of said plant transcription factor.

54. (New) The method of claim 53, wherein the conserved domain comprises:

an amino acid sequence of residues 145-213 of SEQ ID NO: 18;

an amino acid sequence having at least 84% identity to residues 145-213 of SEQ ID NO: 18; or

an amino acid sequence of residues 145-213 of SEQ ID NO: 18 having one or more conservative substitutions, deletions, or insertions.

14 ~~55.~~ (New) The method of claim 13 ~~53~~, wherein the recombinant polynucleotide comprises SEQ ID NO: 17.

15 ~~56.~~ (New) The method of claim 13 ~~53~~, wherein the recombinant polynucleotide further comprises one or more regulatory sequences.

16 ~~57~~. (New) The method of claim 15 ~~56~~, wherein said one or more regulatory sequences are selected from the group consisting of a promoter, a transcription initiation start site, an RNA processing signal, a transcription termination site, and a polyadenylation signal.

17 ~~58~~. (New) The method of claim 16 ~~57~~, wherein the selected promoter is constitutive, inducible, or tissue-specific.

59. (New) The method of claim 53, wherein the nucleotide sequence encodes a polypeptide of SEQ ID NO: 18, wherein expression of the recombinant polynucleotide enhances the plant's tolerance to fungal disease when compared with the same trait of another plant of the same species lacking the recombinant polynucleotide.

60. (New) The transgenic plant of claim 59, wherein said fungal disease is caused by *Fusarium*, *Erysiphe, Sclerotinia* or *Botrytis*.

61. (New) A transgenic plant comprising a recombinant polynucleotide comprising a nucleotide sequence encoding a transcription factor comprising a conserved domain of a plant AP2 transcription factor, wherein:

said nucleotide sequence hybridizes under stringency conditions to a polynucleotide sequence encoding an amino acid sequence of residues 145-213 of the AP2 transcription factor of SEQ ID NO: 18, wherein:

said stringency conditions comprise wash conditions of 0.2 x SSC, 0.1% SDS at 65° C, and wherein:

said transgenic plant is characterized by enhanced tolerance to plant disease due to changes in expression levels or activity of said plant transcription factor.

62. (New) The transgenic plant of claim 61, wherein the recombinant polynucleotide comprises SEQ ID NO: 17.

63. (New) The transgenic plant of claim 61, wherein the recombinant polynucleotide further comprises one or more regulatory sequences.

64. (New) The transgenic plant of claim 63, wherein said one or more regulatory sequences are selected from the group consisting of a promoter, a transcription initiation start site, an RNA processing signal, a transcription termination site, and a polyadenylation signal.

65. (New) The transgenic plant of claim 64, wherein the selected promoter is constitutive, inducible, or tissue-specific.

66. (New) The transgenic plant of claim 61, wherein expression of the recombinant polynucleotide enhances the plant's tolerance to fungal disease when compared with the same trait of another plant lacking the recombinant polynucleotide.

67. (New) The transgenic plant of claim 66, wherein said fungal disease is caused by *Fusarium*, *Erysiphe, Sclerotinia* or *Botrytis*.

68. (New) A method for enhancing the disease tolerance or resistance in a plant comprising transforming said plant with a recombinant polynucleotide comprising a nucleotide sequence encoding a transcription factor comprising a conserved domain of a plant AP2 transcription factor, wherein:

said nucleotide sequence encoding said transcription factor hybridizes under stringency conditions to a polynucleotide sequence encoding a conserved domain comprising an amino acid sequence of residues 145-213 of the AP2 transcription factor of SEQ ID NO: 18, wherein:

said stringency conditions comprise wash conditions of 0.2 x SSC, 0.1% SDS at 65° C, and wherein:

said transgenic plant is characterized by enhanced tolerance to plant disease due to changes in expression levels or activity of said plant transcription factor

69. (New) The method of claim 68, wherein the recombinant polynucleotide comprises SEQ ID NO: 17.

70. (New) The method of claim 68, wherein the recombinant polynucleotide further comprises one or more regulatory sequences.

71. (New) The method of claim 70, wherein said one or more regulatory sequences are selected from the group consisting of a promoter, a transcription initiation start site, an RNA processing signal, a transcription termination site, and a polyadenylation signal.

72. (New) The method of claim 71, wherein the selected promoter is constitutive, inducible, or tissue-specific.

73. (New) The method of claim 68, wherein expression of the recombinant polynucleotide enhances the plant's tolerance to fungal disease when compared with the same trait of another plant of the same species lacking the recombinant polynucleotide.

74. (New) The transgenic plant of claim 73, wherein said fungal disease is caused by *Fusarium*, *Erysiphe, Sclerotinia* or *Botrytis*.

75. (New) A transgenic plant comprising a recombinant polynucleotide encoding a transcription factor of SEQ ID NO: 18, or the same sequence with one or more conservative substitutions, deletions, or insertions, wherein said transgenic plant has enhanced tolerance to fungal disease due to changes in expression levels or activity of said plant transcription factor.

76. (New) The transgenic plant of claim 75, wherein said fungal disease is caused by *Fusarium*, *Erysiphe, Sclerotinia* or *Botrytis*.--